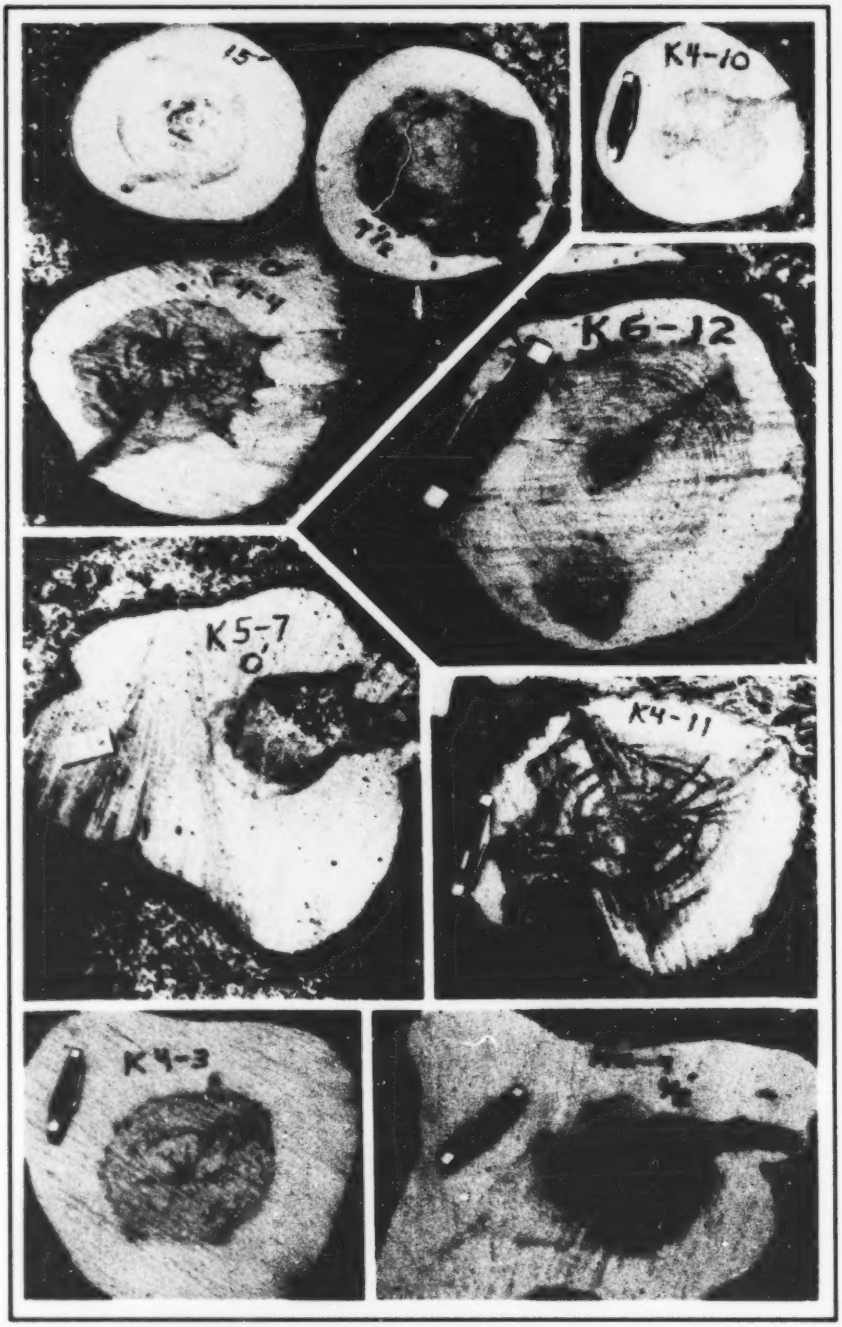
Forest Research Report No. 111

Variations in the Growth and Defect of Aspen (*Populus tremuloides* Michx.) Clones in Northern Ontario



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ABSTRACT

Interclonal variation in trembling aspen (Populus tremuloides Michx.) was investigated for ten clones in each of six stands in northern Ontario. Significant ($p<0.05$) or highly significant ($p<0.01$) interclonal variation was observed in all stands for height, dbh, volume, % bark, % defect, % stain, natural pruning, stub height, and branch diameter; and nonsignificant variation was observed in one or more stands for breast height age, % advanced rot, % incipient rot and number of conks. Broad sense heritability estimates revealed that on the average less than one-third (1/3) of the phenotypic variation was the result of genetic constitution, except for height, % stain, and stub height where it was greater. The occurrence of the 17 wood decay fungi (Hymenomycetes) isolated was equal among clones within a stand in most instances. Fomes igniarius (L. ex. Fr.) Kickx. var. populinus (Nev.) Campb., Radulum casearium (Morg.) Lloyd, Peniophora polygonia (Pers. ex. Fr.) Bourd et Galz, and Armillaria mellea (Vahl ex. Fr.) Kummer occurred frequently and exhibited varying linear trends with age. The occurrence of P. polygonia in one stand appeared to be strongly influenced by its genotype and/or environment. Within the stands studied, 13 site parameters appeared to have little influence on the clonal variables. However, undefined site factors (possibly micro-climatic) appeared to have considerable impact on the % defect in four of the stands. Correlations between variables representing the external clone features and the internal features (stain and decay) were nonsignificant in most cases indicating that the features are probably independent.

Interclonal variation for nine root characteristics was examined in three of the six stands, and was nonsignificant in some cases. Relationships between stem features (dimension and defect statistics) and root characteristics for individual trees were mostly nonsignificant. However, a significant positive relationship between dbh and the number of large roots was very prominent at all levels within the population. Multiple samples in one large clone (0.35 ha) covering three apparent sites showed that only height was significantly different among the samples, and that it was inversely related to % gravel in the B2 horizon but it was suggested that the relationship may not be causal, or the only one. Genetic influences, even though real and nontrivial, play a secondary role in the observed phenotypic variation in trembling aspen in northern Ontario.

INTRODUCTION

Trembling aspen (Populus tremuloides Michx.) regenerates following stand disturbance most frequently by the production of root suckers. In Manitoba, Steneker (1972) found that clones resulting from this asexual mode of reproduction were represented by one to several individuals (ramets) covering less than 0.004 ha (0.01 ac) to numerous individuals covering as much as 1.5 ha (3.8 ac). Kemperman and Barnes (1976) identified clones of 10.1 ha and 43.3 ha in Utah, and estimated from aerial photographs that clones of more than 81 ha were also present. In addition to the large clones, they identified small clones of approximately 0.04 ha along the roadsides. The importance of recognizing the clonal nature of aspen for both management and research has been suggested by several authors (Zahner and Crawford 1965, Wall 1971 and Steneker 1973).

Wall (1971), Steneker (1974) and Kemperman et al. (1978) have suggested that the development of an aspen management system, based on the manipulation of the clonal composition of natural stands, may provide an increase in stand productivity and/or quality. The apparent (phenotypic) variation among aspen clones for morphological characteristics, phenological development, wood and pulp properties, disease susceptibility, and growth characteristics have been examined by many investigators (see Einspahr and Winton 1977 and Kemperman 1977 for summaries of pertinent work). In the preliminary study (Kemperman et al. 1978), the first estimates of clonal variability for growth and defect statistics were obtained for northern Ontario. In this expanded study further documentation of the variability among aspen clones is presented.

OBJECTIVES

1. Determine if significant differences exist among aspen clones within a stand for dimension and defect statistics, and tree characteristics.

2. Assess the influence of site and stand characteristics on the growth and defect of aspen clones.

3. Determine if relationships exist between the external appearance of individual stems and clones, and internal defect.

4. Determine if there are relationships between stem dimension and defect statistics, and root defect and dimension statistics for clones and individual trees.

5. Determine if the level of occurrence of the isolated Hymenomycetes was equal for stands, and clones sampled within stands.

STUDY AREAS AND METHODS

The stands sampled in the study were located in two areas: 1/ the Fort Frances District, Menany Township, and 2/ the Terrace Bay District, American Can of Canada Ltd. license. The Fort Frances District was selected because it contains some of the oldest aspen stands regenerated following logging, and the Terrace Bay District was selected due to the availability of younger aspen stands regenerated following logging and

older stands resulting from wildfire. Stands in both areas were considered representative of northern Ontario. A total of six stands were sampled, three of logging origin and three of wildfire origin. Two stands of logging origin in the 30-year age class were located in the Terrace Bay District (Camp 15, ca. 1948 and Ramsey Lake, ca. 1946). The third stand of logging origin was located in the Fort Frances District (ca. 1940). Stands originating from wildfire were all located in the Terrace Bay District and consisted of one stand in the 60-year age class (Kagiano Lake) and two stands between 100-110 years of age (Stevens and Anthony Lake).

Site variations among clones within a stand were minimized by selecting stands that appeared to be on homogeneous sites. In each of the selected stands, clones were identified and delineated based on morphological (bark) and phenological characteristics (timing and progression of leaf coloration and fall) in the fall, and/or leaf morphology and phenological development (flushing) in the spring. The ten most distinct clones in each area were chosen for sampling and their locations mapped.

A single sample plot was established at the approximate centre of each of the ten sample clones and consisted of the nearest nine dominant and/or codominant trees, and nearest three intermediate trees; this procedure was followed for the Fort Frances, Stevens, Anthony Lake, and Kagiano Lake stands. An exception was clone 9 at Anthony Lake; this was a relatively large clone occurring on a variety of sites. Two additional sample plots (plots 11 and 12) were established in clone 9 to evaluate the effects of site on growth and defect within a single clone and the data for these two additional plots were only considered when examining this one clone. The sampling procedure used for the Camp 15 and Ramsey Lake stands was the same except that twelve dominant-codominant trees and four intermediate trees were sampled. Suppressed trees were not sampled in any of the clones. A total of 800 trees from the six stands was considered the sample population except as noted above.

Prior to felling the sample trees, the stand data and a portion of the individual tree data were obtained. Stand data consisted of the basal area estimated with a 2.3 $m^2.ha^{-1}$ prism (10 $ft^2.ac^{-1}$) tallied in three components (total basal area, total aspen basal area, and total aspen minus suppressed aspen basal area). Sample tree data obtained prior to felling was crown class (1/ dominant, 2/ codominant, and 3/ intermediate); natural pruning class (1/ best 1/3 of stand, 2/ intermediate 1/3 of stand, and 3/ poorest 1/3 of stand) based on the quantity and diameter of dead branches, and large branch stubs; number of Fomes igniarius (L. ex. Fr.) Kickx. var. populinus (Nev.) Campb. conks (0, 1-5, 6-10, 10+); and stub height (estimated height (ft) to the first dead branch 30 cm (1 ft) or more in length).

Each sample tree was felled, and the total height was measured, to the nearest 30 cm (1 ft). The trees were subsequently sectioned at 1.37 m (4.5 ft), 3.05 m (10 ft) and at 1.53 cm (5 ft) intervals to the top. Discoloured wood at the cut surface was tested with a knife for hardness and classified as stain, when it had the hardness of clear wood; incipient rot, when it was slightly softer than clear wood; and advanced rot, when it was appreciably softer than clear wood. At each cut the diameter outside bark, diameter inside bark, and diameter of the stain, incipient rot and advanced rot columns were measured and recorded on logarithmic stem analysis forms, along with the colour of the defect, and

the diameter outside bark (15 cm (6 in) from the bole) of the two lowest live branches. Tree volume inside bark (i.b.), and the volumes of stain, and advanced and incipient rot were determined from the stem analysis forms with a planimeter, with the defect volumes expressed as a percent of the volume (i.b.). Percent defect was the sum of the percent stain, percent advanced rot and percent incipient rot. The end point of defect columns which ran out between cuts were determined by making additional cuts. For each distinctive type of defect that appeared, sample blocks were collected. Two discs, one each at the base and at 1.37 m, were saved for age determination from two dominant-codominant trees and one intermediate tree per clone. All clone ages presented are based on the mean age at breast height (age [bh]) to the nearest year.

Stumps with roots cut to a 30 cm (1 ft) length were excavated for three dominant-codominant trees and one intermediate tree for each of ten clones in the Camp 15 and Ramsey Lake stands; and two dominant-codominant trees for five of the clones in the Fort Frances stand for a total of 90 trees. The root systems were brushed clean of soil and debris, and the parent roots of each tree were identified if possible. The roots were cut approximately 30 cm from their points of origin, and their diameters at these cuts recorded. Roots with diameters of 2 or more cm were classed as large roots, less than 2 cm as small roots. The type and diameter of stain or decay on the cut surfaces, and at cuts made adjacent to the root collar, were recorded. The term root collar refers to the below-ground portion of the stem, in which individual roots are externally indistinguishable. The root collars were subjected to two longitudinal cuts, 90 degrees from one another. These cuts exposed most stains or decays present for descriptions and measurements. Roots and root collars were also examined for the presence of wounds, and for insect boring activity. As in the case of stems, sample blocks of defective root and root collar wood were collected.

The sample blocks of defective wood were used for the isolation of micro-organisms inhabiting, and causing, the defects. This was done by Canadian Forestry Service (CFS) staff in their trailer-laboratory at Ramsey Lake Silvicultural Camp for the Terrace Bay samples, and at the Great Lakes Forest Research Centre (GLFRC), Sault Ste. Marie, for the Fort Frances samples. Any samples that were not processed within ten days after being cut were placed in a cold room from that point on to maintain organism viability and reduce the danger of contamination. Isolation attempts were made by aseptically removing small bits of defective wood, about 5 x 2 x 2 mm, from freshly exposed surfaces and placing them in test tubes containing 2% malt agar. The test tubes were incubated at GLFRC until micro-organisms covered the agar surface, at which time they were identified.

The results of the isolation attempts were reduced prior to analysis by tallying the occurrence of an organism or nonoccurrence (e.g. sterile) only once for each clone and tree even when successive attempts from the same clone or tree yielded identical results. In the case of Fomes igniarius, some counts were based on the presence of conks on the tree, or the distinctive pattern and colour of the decay (Basham 1958), and no isolation attempts were necessary. A contingency chi-square was used to test for differences in the frequency of occurrence of individual Hymenomycetes among clones within stands, and among stands for groups of trees.

Soil and site information obtained for each clone included the aspect (eight cardinal points), percent slope, and rooting depth (cm). Soil samples were taken from the B2 and C horizons for determination of the percent gravel, pH, and the percent of sand, silt and clay (hydrometer method).

Interclonal variation, for all stem and root statistics, was evaluated using an analysis of variance. Similarly, analysis of variance was used to determine if significant intraclonal variation existed for the stem statistics in one large clone at Anthony Lake (clone 9, and plots 11 and 12). For each of the six stands broad sense heritability estimates were determined for all stem statistics as described by Zsuffa (1975). Pearson correlation coefficients (Nie et al. 1975) were determined for various combinations of stand, stem and root statistics for the clones within and among stands to elucidate possible linear trends in the data. Multiple linear regression (Raymond 1980) was used to evaluate possible colinear relationships between independent variables.

RESULTS AND DISCUSSION

Mycological Data

Approximately 6,000 isolation attempts were made from the 800 trees representing the 60 clones in this study. In many of the test tubes two or three organisms were identified. No attempt was made to determine if these combinations were important in the development of defect, as it was considered beyond the scope of this study.

Results of the isolation attempts for clones and trees by stand and the total sample population are summarized in Table 1. It is apparent, from Table 1, that all clones and a majority of the trees contain one or more micro-organisms. In fact no tree was found to be free of micro-organisms. Many of the isolated organisms are of little or no importance in the development of decay (bacteria and yeasts [Basham and Navratil 1975]), or play relatively minor roles (Ascomycetes and Fungi Imperfecti [Deuteromycetes]). It is possible that some of these organisms may cause limited wood discolouration (stain). There is evidence that a few of them can precede decay, possibly making the substrate more suitable for the decay-causing Hymenomycetes. With one or two exceptions, only the Hymenomycete group of fungi are capable of causing decay in living trees, and these are the organisms that will be emphasized in this report.

Seventeen Hymenomycetes were isolated from the defect samples. All of these had been isolated from stem decay in aspen previously, in two studies carried out in mature aspen stands of wildfire origin in Ontario in the 1950s (Basham 1958, Basham and Morawski 1964). Although clones were not considered in those studies, a total of 4,212 trees were involved, and the following summaries of the effects and importance of the 17 Hymenomycetes within the stems of living aspen are based largely on those two studies. The fungi are discussed more or less in order of their importance and impact; some have recently proposed new names in parentheses.

TABLE 1 Results of isolation attempts indicating presence of micro-organisms in clones and trees, by area

	Camp 15		Ramsey Lake		Fort Frances		Kagiano Lake		Stevens		Anthony Lake		Total	
	Clones	Trees	Clones	Trees	Clones	Trees	Clones	Trees	Clones	Trees	Clones	Trees	Clones	Trees
	(10)	(160)	(10)	(160)	(10)	(120)	(10)	(120)	(10)	(120)	(10)	(120)	(60)	(800)
Sterile	10	135	10	158	10	120	10	90	10	74	10	78	60	655
Bacteria	10	106	10	150	10	95	10	82	10	58	10	82	60	573
Unidentified Fungi Imperfecti	10	97	10	111	10	80	10	65	10	96	10	107	60	556
Phialophora alba	10	54	10	54	10	78	10	82	10	94	10	82	60	444
Peniophora polygonia*	10	105	10	98	9	33	10	61	8	17	10	36	57	350
Yeasts	10	68	10	105	10	79	8	24	6	11	9	25	53	312
Ascocoryne sarcoides	7	19	10	31	5	12	9	16	8	30	10	20	49	128
Fomes igniarius*	1	1	0	0	5	7	7	16	10	49	10	47	33	120
Armillaria mellea*	4	5	4	5	3	5	9	27	8	21	10	44	38	107
Penicillium thomii	8	34	7	8	7	14	1	3	6	8	9	21	38	88
Libertella spp.	2	2	0	0	1	1	7	10	9	31	8	41	27	85
Radulum casearium*	0	0	2	3	0	0	5	9	10	23	9	43	26	78
Geniculosporium sp.	0	0	1	1	0	0	5	17	8	15	9	19	23	52
Torula spp.	9	23	8	22	2	3	0	0	0	0	0	0	19	48
Phialophora spp.	0	0	0	0	0	0	9	23	3	11	2	2	14	36
Pholiota spectabilis*	0	0	0	0	0	0	1	1	7	18	5	10	13	29
Phycomycetes	1	1	0	0	3	5	1	1	7	21	1	1	13	29
Cytospora sp.	5	8	5	7	5	11	0	0	1	1	1	1	17	28
Unidentified Hymenomycetes*	0	0	0	0	0	0	7	11	6	10	3	6	16	27
Trichocladium canadense	0	0	3	3	0	0	4	5	3	7	6	6	16	21
Trichoderma viride	0	0	1	1	6	9	2	3	1	1	5	7	15	21
Actinomycetes	1	1	4	5	0	0	4	4	6	7	2	2	17	19
Phlebia strigoso-zonata*	3	3	4	4	1	3	1	1	0	0	0	0	9	11
Rhinocladiella spp.	0	0	0	0	0	0	6	7	1	1	2	3	9	11
Pholiota aurivella*	1	1	1	1	2	2	1	1	0	0	3	4	8	9
Verticillium sp. 2	2	2	4	4	0	0	2	2	0	0	0	0	8	8
Polyporus adustus*	0	0	0	0	0	0	1	1	2	2	4	4	7	7
Polyporus zonatus complex*	0	0	0	0	0	0	1	1	4	5	1	1	6	7
Graphium spp.	0	0	0	0	0	0	1	1	1	1	4	4	6	6
Flammula alnicola*	0	0	0	0	0	0	0	0	1	1	3	5	4	6
Coprinus micaceus*	0	0	0	0	0	0	0	0	3	6	0	0	3	6
Leptographium spp. complex	0	0	0	0	0	0	0	0	1	1	3	3	4	4
Gloeocystidiellum karstenii*	0	0	0	0	0	0	0	0	3	4	0	0	3	4
Cephalosporium spp.	0	0	0	0	0	0	2	2	1	1	0	0	3	3
Collybia velutipes*	0	0	0	0	0	0	2	2	0	0	1	1	3	3
Fusidium sp.	0	0	0	0	0	0	2	2	1	1	0	0	3	3
Phoma sp.	0	0	0	0	0	0	2	2	0	0	1	1	3	3
Paecilomyces sp.	0	0	1	1	0	0	1	1	0	0	0	0	2	2
Alternaria sp.	1	1	0	0	0	0	0	0	0	0	0	0	1	1
Arthrobotrys sp.	0	0	0	0	0	0	0	0	1	1	0	0	1	1
Bispora sp.	0	0	1	1	0	0	0	0	0	0	0	0	1	1
Cladosporium sp.	0	0	0	0	0	0	0	0	1	1	0	0	1	1
Nodulisporium sp. 1	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Peniophora cinerea*	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Phomopsis sp.	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Pleurotus ostreatus*	0	0	0	0	0	0	0	0	1	1	0	0	1	1
Scytinostroma galactinum*	0	0	0	0	0	0	1	1	0	0	0	0	1	1
Stereum purpureum*	0	0	0	0	0	0	0	0	0	0	1	1	1	1
Thysanophora sp.	0	0	0	0	0	0	1	1	0	0	0	0	1	1

* indicates a Hymenomycete

Fomes igniarius var. populinus (= Phellinus tremulae Bond. et Boris) is by far the most serious cause of stem decay in aspen. It causes a yellowish-white trunk or butt decay with characteristic black zone lines; its texture varies from fairly firm to punky or spongy, depending on the stage of decay. Trees with extensive columns of decay usually have conspicuous hoof-shaped conks (fruiting bodies) of the fungus on the trunk. It seldom occurs in trees younger than 30 years of age; after that it generally becomes increasingly important with tree age.

Radulum casearium (Morg.) Lloyd is associated with a yellow stringy trunk and butt decay. Fruiting bodies are seldom formed on living trees. It is seldom isolated from trees younger than 60 years of age, but is responsible for considerable defect in aspen more than 90 years old.

Peniophora polygonia (Pers. ex. Fr.) Bourd. et Galz, (= Cryptochaete polygonia [Fr.] Karst.) is the Hymenomycete most frequently isolated from aspen younger than 40 years of age, but is seldom found in trees older than 100. It is usually isolated from firm, stained wood, or a yellowish-white fairly firm (incipient) decay.

The next seven Hymenomycetes, listed in order of their frequency of occurrence, and importance, in trembling aspen, are associated with yellow-orange stringy butt decays. They are Armillaria mellea (Vahl ex. Fr.) Kummer, Pholiota spectabilis (Fr.) Kummer, Pholiota aurivella (Batsch ex. Fr.) Kummer, Collybia velutipes Curt. ex. Fr., Coprinus micaceus Fr., Flammula alnicola (Fr.) Kummer, and Corticium galactinum (= Scytinostroma galactinum (Fr.) Donk). These fungi are more important than their volumes of stem decay would indicate, because they occur in the root systems as well and are responsible for windthrow, increment reductions, and occasionally tree mortality. The occurrence of A. mellea in individual aspen trees is far higher than the frequency with which it is isolated from stems would indicate, since it is known to occur extensively in aspen root systems without extending above ground level. This probably applies to a lesser extent to some or all of the six other butt decay fungi.

The remaining seven Hymenomycetes isolated in this study are relatively rare and unimportant, and can be divided into two groups. The first group, which includes Gloeocystidiellum Karstenii (Bourd. et Galz.) Donk. Peniophora cinerea (Fr.) Cke., and Pleurotus ostreatus Jacq. ex. Fr., occur occasionally in yellow-orange stringy trunk or butt decays of aspen. The second group, composed of Polyporus adustus Willd. ex. Fr., Polyporus zonatus Fr., Stereum purpureum (Pers. ex. Fr.) Fr. and Phlebia strigoso-zonata (Schw.) Lloyd, are generally associated with the decay of sapwood (sap rot) in dead aspen trees. Their occurrence in the stems of living trees is almost invariably as small patches of sap rot associated with various types of stem wounds that results in localized death of the cambium and adjacent xylem tissue.

Occurrence of Hymenomycetes

In examining the Hymenomycete data two questions were set forth: 1/ are there differences in the level of occurrence among stands for groups of trees that would suggest the influence of stand age, or site conditions (soil, topography or local climate) on pathogen occurrence; and 2/ are there differences among clones within a stand that would

indicate possible resistance, due to genotype and/or micro-site, against the specific Hymenomycetes.

Regarding the influence of stand age or site conditions on the level of occurrence of Hymenomycetes there are a few general trends in the data. The sum of occurrences for all Hymenomycetes tends to be positively related to stand age. Within a given age class (+/- 5 years), the sum of occurrences seem to be inversely related to site quality in the young stands (Camp 15, Ramsey Lake and Fort Frances) and possibly directly related to site quality in the overmature stands (Stevens and Anthony Lake). The sample sizes three and two upon which these possible trends are based are too small to be very confident; however, the same trends seem to exist within an age class when all organisms are considered.

Nonsignificant differences in the frequency of occurrence of individual Hymenomycetes among stands for groups of trees were obtained for Peniophora cinerea, Pleurotus ostreatus, Scytinostroma galactinum, Stereum purpureum, Collybia velutipes, Pholiota aurivella, and Phlebia strigoso-zonata (Table 2). The nonsignificant differences among stands for trees indicates a constant level of occurrence for these organisms within the sample populations. None of these fungi occurred in more than 11 of the 800 sample trees (Table 1), suggesting that they occur infrequently due to a combination of unfavourable site conditions and an inherent biological trait of infrequent fruiting-body production; or that they are abundant, but of low virulence; or that aspen has a high degree of resistance towards them. It is notable that the ratio occurrence (frequency of occurrence/sample size) for Phlebia strigoso-zonata was significantly ($p<0.05$) inversely related to stand age.

The remaining ten Hymenomycetes had statistically significant differences among stands for groups of trees. Statistically significant differences in the levels of occurrence among stands for groups of trees indicates that the stands differ in composition, and the reasons for these differences are probably differences in stand age or site conditions. Gloeocystidiellum Karstenii and Coprinus micaceus were isolated only in the Stevens stand. In this instance it is suggested that site conditions were probably the main factors contributing to the occurrence of these pathogens. In contrast, the differences in the occurrence of Flammula alnicola, Polyporus zonatus complex. Polyporus adustus, Pholiota spectabilis, Radulum casearium, Armillaria mellea, Fomes igniarius, and Peniophora polygonia appear to be influenced primarily by stand age. F. alnicola only occurred in the two overmature stands (Stevens and Anthony Lake); P. zonatus complex. P. adustus, and P. spectabilis occurred only in the mature to overmature stands; and the four most frequently occurring Hymenomycetes (R. casearium, A. mellea, F. igniarius, and P. polygonia) exhibited varying linear trends with stand age.

For P. polygonia there is an inverse relationship between the ratio of occurrence (frequency of occurrence/sample size) and stand age, and some apparent variability arising from variations in pathogen genotype or site conditions (soil, topography, and/or local climate). The linear correlation for the ratio of occurrence and stand age relationship is $r = -.95$ for the five stands sampled in the Terrace Bay District. The ratio of occurrence for the Fort Frances stand is between the lower bounds of the 95% and 99% confidence intervals for the regression line of the Terrace Bay stands, suggesting that it is on the fringe of the

TABLE 2 Results of the contingency Chi-square for the level of occurrence of specific Hymenomycetes between clones within stand and between stands

Hymenomycete	Camp 15	Ramsey Lake	Fort Frances	Kagiano Lake	Stevens	Anthony Lake	Population
Peniophora polygonia	NS[1]	*[2]	**[3]	NS	NS	*	**
Fomes igniarius	NS	--[4]	NS	NS	NS	NS	**
Armillaria mellea	NS	NS	*	NS	**	NS	**
Radulum casearium	--	*	--	NS	NS	**	**
Pholiota spectabilis	--	--	--	NS	*	*	**
Phlebia strigoso-zonata	NS	NS	**	NS	--	--	NS
Pholiota aurivella	NS	NS	NS	NS	--	NS	NS
Polyporus adustus	--	--	--	NS	NS	NS	*
Polyporus zonatus complex	--	--	--	NS	NS	NS	**
Flammula alnicola	--	--	--	--	NS	NS	**
Coprinus micaceus	--	--	--	--	NS	--	**
Gloeocystidiellum karstenii	--	--	--	--	NS	--	**
Collybia velutipes	--	--	--	NS	--	NS	NS
Peniophora cinerea	--	--	--	--	--	NS	NS
Pleurotus ostreatus	--	--	--	NS	--	--	NS
Scytinostroma galactinum	--	--	--	--	--	NS	NS
Stereum purpureum	--	--	--	NS	--	--	NS

1 - nonsignificant
2 - significant at the 0.05 level of probability
3 - significant at the 0.01 level of probability
4 - not tested, Hymenomycete not isolated

population. The distance (approx. 650 km) separating the Fort Frances stand and Terrace Bay stands suggests differences resulting from variaton in local climate, genotypic variation in P. polygonia, or an interaction of local climate and genotype. Genotypic variation and interaction with local climate are the most likely causes of wide divergence for the level of P. polygonia in the Fort Frances stand, since the three other most frequently occurring Hymenomycetes occurred at the same levels in the Fort Frances stand as in the Camp 15 and Ramsey Lake stands which are of similar age. However, it must be pointed out that these three Hymenomycetes exhibited positive, but varying linear trends with stand age, and as a result occur infrequently in young stands. At low levels of occurrence only stands having exceptionally high levels of occurrence would be detected as being a different population as the lower limit of the confidence intervals would be zero (0). If the difference in P. polygonia occurrence at Fort Frances is the result of the factors mentioned then one would have to wait until the stands are older to determine if similar patterns in the levels of the other three Hymenomycetes would develop.

Analysis of the Hymenomycete data for variations in the level of occurrence within a stand (among clones) revealed significant differences within a stand or stands for Phlebia strigoso-zonata, Pholiota spectabilis, Radulum casearium, Armillaria mellea, and Peniophora polygonia. Significant differences suggest that one or more of the clones may have partial resistance to the specific pathogen resulting from genetic constitution, micro-site conditions, or an interaction of the two factors. To properly evaluate resistance, controlled inoculations must be carried out on selected clones on a variety of sites. The majority of the comparisons resulted in nonsignificant differences which suggests the level of incidence of specific decay fungi is the same (equal) for all clones within a single stand.

Fungi with high levels of occurrence would suggest little or no host resistance attributable to genotype or site, the presence of abundant pathogen inoculum, and suitable conditions for infection and spread of the pathogens. Low incidence, however, does not necessarily imply a greater degree of host resistance; it could result from a low level of pathogen inoculum and/or unfavourable conditions for infection and spread within the host. It must be stressed that failure to isolate a specific fungus from a tree is by no means proof that fungus was not present in that tree. Although fungi generally thoroughly permeate the tissues enough to alter its appearance that it can be described as a defect, the fact that only a few representative wood chips, roughly 5 x 2 x 2 mm in size, are inserted in test tubes from each defect introduces the possibility that no viable fungal material happened to be present in those chips. Other possible reasons for misleading nonoccurrences are contamination by other organisms of the chips or test tubes, and the replacement with time of decay-causing fungi by other secondary fungi.

A highly significant ($p<0.01$) difference in the level of occurrence for P. strigoso-zonata was obtained for the clones in the Fort Frances stand. This difference was the result of three occurrences, associated with stem wounds, in one clone. As previously stated, P. strigoso-zonata rarely occurs in living aspen and is usually associated with stem wounds. In the other two middle-aged stands (Camp 15 and Ramsey Lake) this organism was restricted to one occurrence in each of the affected clones. The relatively high occurrence in the single clone was possibly

due to the genotype of the clone, or an interaction between genotype and site conditions which may have attributed to stem wounding.

Pholiota spectabilis occurrence was significantly different among the clones in the 100- to 110-year-old Stevens and Anthony Lake stands. In both stands there were clones that had three or more occurrences and more than one-half of the clones had at least one occurrence. As stated previously the occurrence of P. spectabilis appears to be dependent on stand age. It is apparent from the levels of occurrence in the clones of these stands that site conditions are responsible in part. The lower quality Stevens site had nearly twice the number of occurrences per infected clone compared to the Anthony Lake stand. The absence of P. spectabilis in several clones in each stand suggests that there may be resistance in aspen to this pathogen, and that this resistance may be independent of site quality or other site conditions based upon the apparent random distribution among the clones sampled in these two stands; however, this point must be viewed cautiously as P. spectabilis, a butt rot fungus, tends to occur in patches rather than being evenly distributed throughout a stand. The reversal in the relationship between level of occurrence and site quality from the general trend for Hymenomycetes, that occurrence is positively related to site quality in the overmature stands, illustrates the importance of the specificity of each organism for particular conditions that will allow it to flourish.

Of the four most frequently occurring Hymenomycetes significant differences among clones within a stand were obtained in two or more stands for Radulum casearium, Armillaria mellea, and Peniophora polygonia. Fomes igniarius showed no significant differences between clones in any of the stands. As stated previously, F. igniarius is the most serious cause of stem decay in aspen. The lack of significant differences among clones would suggest that resistance, or lack of it, is constant throughout the population, and the possibility of improvement (i.e. reducing occurrence by identifying resistant clones) is unlikely. However, it is possible that resistance to the spread of F. igniarius after infection is different among clones and offers a possible avenue for reducing the impact of this pathogen.

Clone Dimension and Defect Statistics

Two basic questions were asked when examining the dimension and defect statistics. Are there real differences among the clones in a stand for mensurational and defect statistics? Are there any meaningful relationships among these characteristics? Table 3 summarizes the data by area (stand) and lists the result of the analysis of variance for each characteristic.

Age estimates within clones varied a maximum of 11 years (Anthony Lake, Clone 5) and averaged 2 years for the 60 clones. Age estimates among clones within a stand varied a maximum of 13 years (Stevens) and averaged 5 years for the six stands. Significant interclonal age variation was obtained for the two overmature stands, Stevens and Anthony Lake. Variations of up to four years in the breast height age within and between clones, as was found for the four stands with nonsignificant variation, is well within what may be expected. Horton and Maini (1964) determined that 63% of aspen suckers were produced the first year following harvest and 20% during the following two years based on a random sample in a single stand. The large variation in age

TABLE 3 Area means and range in clone means for clone age, tree dimension and defect statistics and the results of analysis of variance

Statistic	Camp 15 Area mean	Range: clone means	F-test sig.
Age (bh)	27	24 - 28	NS1
Ht. (m)	12.0	10.4 - 14.4	**2
Dbh (cm)	9.8	8.5 - 11.0	**
Volume (dm^3)	46	29 - 63	**
% Bark	15.3	13.4 - 18.2	*3
% Defect	11.78	4.83 - 18.02	**
% Advanced rot	0.64	0.08 - 1.51	*
% Incipient rot	1.20	0.23 - 3.03	**
% Stain	9.94	4.44 - 16.94	**

Statistic	Fort Frances Area mean	Range: clone means	F-test sig.
Age (bh)	33	32 - 35	NS
Ht. (m)	20.4	18.8 - 23.1	**
Dbh (cm)	17.4	15.1 - 22.4	**
Volume (dm^3)	232	160 - 418	**
% Bark	13.3	11.9 - 15.9	**
% Defect	17.33	9.03 - 24.03	**
% Advanced rot	1.23	0.09 - 2.84	NS
% Incipient rot	0.52	0.07 - 1.34	*
% Stain	15.58	8.82 - 22.75	**

Statistic	Ramsey Lake Area mean	Range: clone means	F-test sig.
Age (bh)	29	29 - 30	NS
Ht. (m)	12.9	11.9 - 15.0	**
Dbh (cm)	12.2	10.0 - 14.5	**
Volume (dm^3)	76	50 - 112	**
% Bark	12.7	11.0 - 13.7	**
% Defect	13.10	8.21 - 17.44	**
% Advanced rot	0.21	0.02 - 1.06	**
% Incipient rot	1.14	0.31 - 2.24	NS
% Stain	11.75	7.88 - 16.23	**

Statistic	Kagiano Lake Area mean	Range: clone means	F-test sig.
Age (bh)	64	62 - 66	NS
Ht. (m)	25.2	22.6 - 28.2	**
Dbh (cm)	23.6	19.9 - 28.2	**
Volume (dm^3)	550	328 - 776	**
% Bark	12.3	11.2 - 13.7	**
% Defect	22.05	13.53 - 34.77	**
% Advanced rot	1.21	0.13 - 4.99	NS
% Incipient rot	2.99	0.71 - 6.23	**
% Stain	17.85	9.23 - 31.69	**

TABLE 3 Area means and range in clone means for clone age, tree dimension and defect statistics and the results of analysis of variance (cont'd)

Statistic	Stevens Area mean	Stevens Range: clone means	Stevens F-test sig.	Statistic	Anthony Lake Area mean	Anthony Lake Range: clone means	Anthony Lake F-test sig.
Age (bh)	105	99 - 112	**	Age (bh)	106	102 - 110	**
Ht. (m)	23.6	21.8 - 25.2	**	Ht. (m)	27.8	24.3 - 29.6	**
Dbh (cm)	27.7	24.1 - 30.0	**	Dbh (cm)	28.4	24.0 - 33.0	**
Volume (dm^3)	641	464 - 773	**	Volume (dm^3)	826	520 - 1218	**
% Bark	16.6	14.2 - 21.3	**	% Bark	15.2	13.0 - 18.3	**
% Defect	34.80	23.08 - 45.59	**	% Defect	28.86	14.56 - 43.16	**
% Advanced rot	6.94	2.57 - 16.37	**	% Advanced rot	4.42	1.12 - 8.26	*
% Incipient rot	6.22	2.47 - 10.08	*	% Incipient rot	5.58	1.40 - 8.46	**
% Stain	21.65	12.60 - 28.90	**	% Stain	18.86	9.63 - 27.64	**

1 - nonsignificant
2 - significant at the 0.01 level of probability
3 - significant at the 0.05 level of probability

determinations among clones for the two overmature stands may have resulted from at least four possible sources: 1/ natural variation in the suckering process, as stated above, 2/ partial rings, 3/ false rings, and 4/ nondistinguishable rings of unknown cause. False rings are fairly common in aspen. Maini and Coupland (1964) found as many as eight false rings within an increment in prairie grown aspen, and Campbell (1981) citing Glock (Glock, W.S. 1937. Principles and method of tree ring analysis. Carnegie Institution of Washington, Washington, D.C. 100 p.) states that biannual precipitation pattern may result in false rings. The occurrence of periods of drought in northwestern Ontario during the growing season occur with some regularity. It is suspected that false rings and nondistinguishable rings were the major causes of the variation encountered.

The clonal mean percent of the inside bark volume affected by defect varied between 11.78 and 34.80% for the six stands. The greatest portion of the defect was associated with stain and ranged from 9.99 to 21.65% of the volume (i.b.). Incipient rot and advanced rot varied from 0.52 to 6.27% and 0.21 to 6.94%, respectively. The general trend in the magnitude of the three defect components in decreasing order are stain, incipient rot, and advanced rot; however, for the Fort Frances and Stevens stands advanced rot accounted for slightly more (0.7%) of the stem volume than incipient rot. Within the population (800 trees) as a whole, the percent defect and its components tended to be directly related to crown class. This same tendency was exhibited for stands and clones within a stand in many instances, but it was not universal, confirming the results of the preliminary study (Kemperman et al. 1978).

Clonal mean height, diameter breast height (dbh), volume (i.b.), and percent bark, for the six stands, varied from 12.0 to 27.8 m, 9.8 to 28.4 cm, 46 to 826 dm^3, and 12.9 to 16.6%, respectively. Height, dbh, and volume (i.b.) were inversely related to crown class for the stand and total populations, as would be expected. Percent bark was directly related to crown class for the population and for the stand populations, except in the two overmature stands where there was a smaller range in the percent bark and no apparent relationship between bark and crown class.

Interclonal variation for the percent defect and percent stain was found to be highly significant ($p<0.01$) in all six stands. The percent incipient rot exhibited significant ($p<0.05$) interclonal variation in all but the Ramsey Lake stand; while interclonal variation for advanced rot was significant only for the Camp 15, Ramsey Lake, Stevens and Anthony Lake stands. Within stand interclonal variation for the four dimension statistics was statistically highly significant in all cases. These results are not surprising considering the results of the preliminary study (Kemperman et al. 1978) and the results of other studies dealing with interclonal variation (Jones and Trujillo 1975, Steneker 1972, Wall 1971, Barnes 1969, Einsphar and Benson 1967, and Zahner and Crawford 1965).

Even though there is significant interclonal variation for the percent defect, percent stain and dimension statistics, and as will be shown later for the tree characteristics, the portions attributable to genotype and environment are confounded (i.e. all genotypes are not grown in the same environment) when studying clones in a natural stand. Broad sense heritability estimates based on natural stand data are most likely to be overestimates of the true value and statistically incorrect, as

pointed out by Barnes (1969). By definition, the tree to tree variation within a clone is due entirely to environment, and the variation between clones is due to genetic constitution and environment (Buijtenen et al. 1959). Broad sense heritability is the ratio of genetic variance to the total phenotypic variance (genetic and environmental variance), and is determined by portioning the variance components from the analysis of variance as follows (Zsuffa 1975):

$$h^2 \text{ (broad sense heritability)} = \frac{\sigma^2 C}{\sigma^2 C + \sigma^2 E}$$

where $\sigma^2 E$ = error mean square and

$$\sigma^2 C = \frac{\text{clone mean square - error mean square}}{\text{number of stems per clone}}$$

It is usually assumed that the environmental variation will be minimized by selecting sample areas that appear homogeneous with respect to soil and topography. A graphical attempt was made to validate the hypothesis that the clone location within the stands sampled did not influence the phenotypic expression for the stem dimension and defect statistics. The five clones having the smallest mean percent defect, and the greatest mean dbh, volume (i.b.) and height were circled on scale drawings and subjectively evaluated for the presence of patterns. It was assumed that the selected clones would be distributed at random and not grouped in one section of the stand or lined parallel to any "site" feature. The results are particularly revealing for the percent defect in the Camp 15 and Ramsey Lake stands in that a prominent pattern is apparent.

For the Camp 15 stand the five least defective clones were numbers 1, 2, 3, 6 and 10 (Figure 1). Of these, clones 1, 2, 3 and 6 were all located near the stand edge parallel to a main haul road. Similarly, for the least defective clones (numbers 1 to 5) in the Ramsey Lake stand (Figure 2), four were located near the stand edge parallel to a main haul road. The observed pattern does not appear to be related to the soil or topographic data. At the beginning of the study, these factors were believed to be important, but the range in these factors is in most cases described by the five sample points selected, suggesting perhaps that micro-climatic (or other) parameters were more influential. In the Kagiano Lake and Stevens stands four of the five least defective clones were grouped in the one section of the study areas, but not in relation to any observed site or topographic feature. The two remaining stands (Fort Frances and Anthony Lake) showed only moderate grouping (2 groups), unrelated to site or topography. For the dimension statistics considered, groupings were not apparent. except for volume (i.b.) in the Stevens and Anthony Lake stands.

Heritabilities were calculated for the dimension and defect statistics knowing that they are overestimates and statistically invalid. However, it was felt that they give a rough estimate of what may be expected as a maximum upper limit for the stands sampled. Heritabilities, like other statistics, are subject to sampling variation, and this variation was very evident in the range of values obtained (Table 4). For the majority of the dimension and defect statistics the environmental influence, on the average, accounts for the largest portion of the variation suggesting that the variation due to genotype though significant may not be as important as that due to environmental

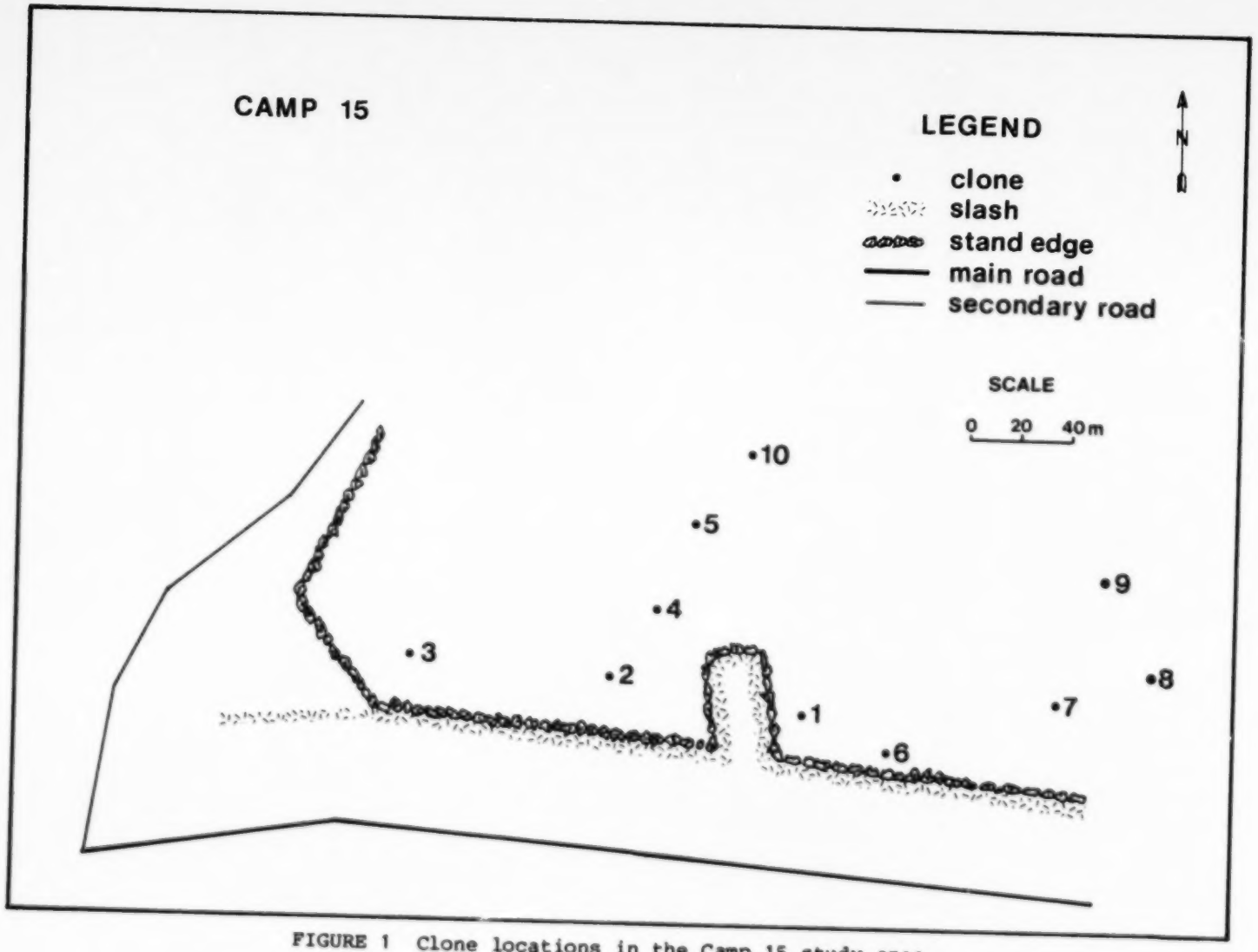

FIGURE 1 Clone locations in the Camp 15 study area.

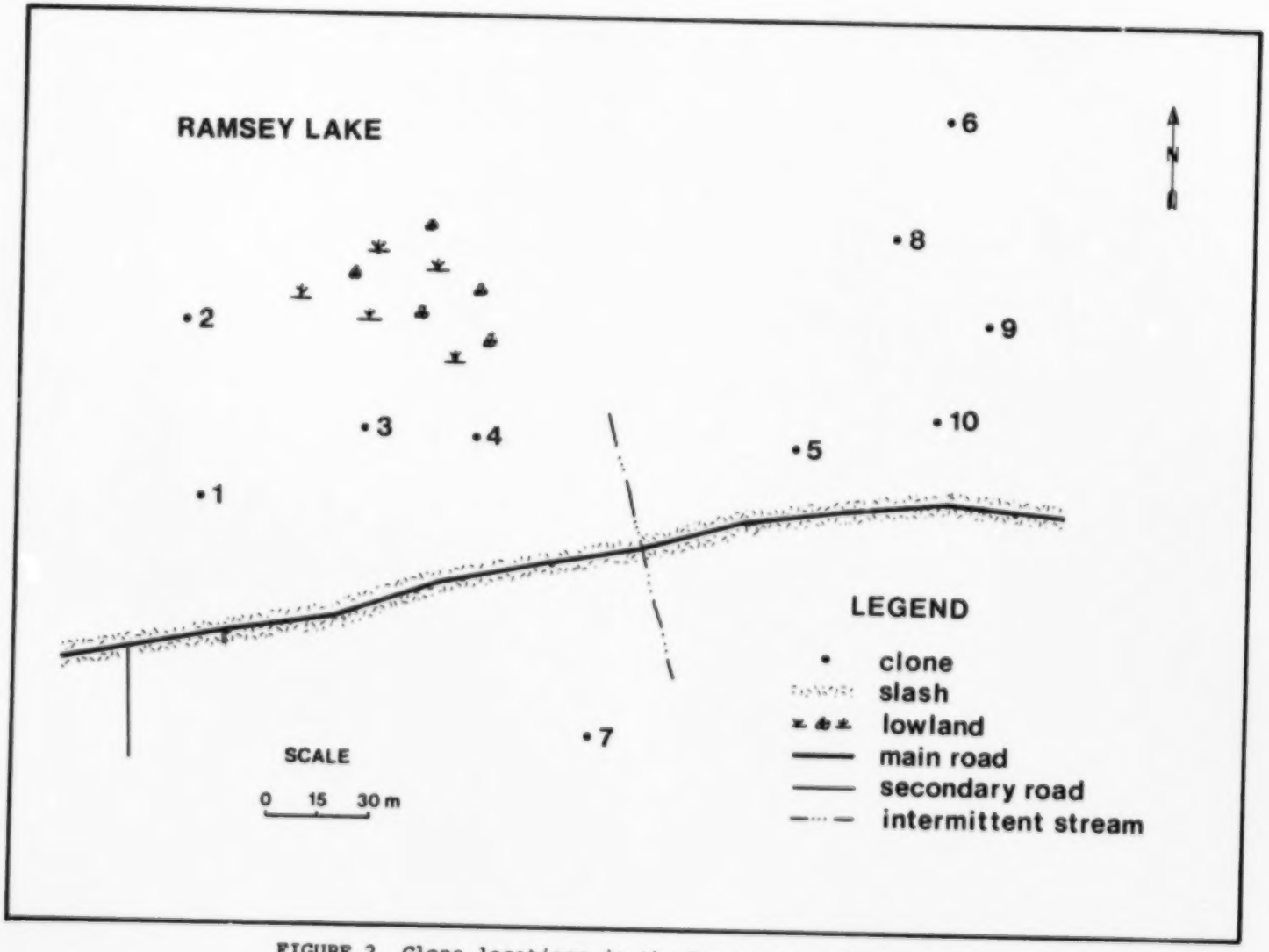

FIGURE 2 Clone locations in the Ramsey Lake study area.

TABLE 4 Mean and range of heritabilities for the dimension and defect statistics for the six stands sampled

Statistic	Mean	Range
Total height	0.58	0.31 - 0.80
Dbh	0.20	0.13 - 0.23
Volume	0.26	0.18 - 0.33
% Bark	0.30	0.08 - 0.61
% Defect	0.32	0.19 - 0.50
% Advanced rot	0.11	0.02 - 0.27
% Incipient rot	0.15	0.02 - 0.35
% Stain	0.39	0.22 - 0.60

factors. However, the environmental factors responsible have not been identified and probably represent a dynamic process rather than independent single factors. Rowe (1964) supports the idea that environmental conditioning influences the phenotypic expression and presents a reference to an asexually reproduced species (potatoes) which indicates that an environmental effect can be traced back as far as the grandparent generation.

Pearson correlations were calculated to determine if there were significant linear correlations in the 60 clone population between clone dimension and defect statistics. All significant correlations were positive indicating that the variables were directly proportional. The most prominent variable was clone age. The linear trend with age would account for 50% or more of the variation in height, dbh, volume (i.b.), percent defect, and percent incipient rot for the population. Correlations between the defect statistics and the three typical mensurational statistics (height, dbh, and volume) were all significant and the strongest were between dbh, and the percent defect and its components. The percent bark resulted in the weakest correlations with the other variables, but significant correlations were present for the percent bark with clone age, percent advanced rot, percent defect and percent incipient rot in descending order of importance. It is important to realize that the significant correlations between the dimension and defect statistics may be spurious due to colinearity with age which accounts for at least 50% of the variation within the population for the stated variables. Results of multiple linear regression indicate that the addition of each dimension statistic as an independent variable after fitting age with the defect statistics would not significantly reduce the error term indicating that correlation between dimension and defect statistics are spurious.

Correlation between the dimension and defect statistics among clones within the individual stands resulted in seven significant coefficients. In the Camp 15 stand the % bark was directly related (positive slope) to the percent defect and percent stain at the 0.05 level of probability and inversely related (negative slope) to height at the 0.01 level of probability. Height was directly related to percent advanced rot and percent incipient rot, and dbh was directly related to percent incipient rot in the Ramsey Lake stand. The final significant correlation was for the percent bark and height in the Anthony Lake stand. Judging from the

low frequency of significant correlations there are no general all encompassing relationships between the dimension and defect statistics among clones within a stand. That is, the clonal dimension statistics are independent of the defect statistics.

Tree Characteristics and Defect

As in the previous section, the tree characteristics were analyzed to determine if there was significant variation between the clones within a stand, and if there were linear trends between the tree characteristics and the defect variables. A summary of the tree characteristic statistics and the results of the analyses of variance are presented in Table 5.

Natural pruning varied between 1.2 and 2.8 for the 60 clones, and was inversely related to all dimension and defect statistics. Stub height ranged from 1.7 to 13.2 m, and was positively correlated to the dimension and defect statistics. Branch diameter, and number of conks per tree had the following ranges for the 60 clone samples, 1.7 to 9.4 cm, and 0 to 2.1, respectively. Branch diameter, and number of conks were positively correlated with the dimension and defect statistics. All of the correlation coefficients were significant except for natural pruning with percent defect, percent advanced rot and percent stain. As with the previous set of correlations using the 60 clone population, age, though not examined statistically, was the underlying force in the correlations. The tree characteristics add nothing to the information about the relationships of the general clonal population and defect was not apparent in the previous comparisons.

Interclonal variation, within a stand, was highly significant for natural pruning, stub height, and branch diameter in all stands suggesting that there is strong genetic control over these factors. However, as with the dimension and defect statistics heritabilities were fairly low. Mean heritabilities for these characters were 0.28 (natural pruning), 0.37 (stub height), and 0.20 (branch diameter). The number of conks varied significantly only for the clones in the Stevens stand, and there were no conks present for the clones sampled in the two youngest stands (Camp 15 and Ramsey Lake). The presence of only one significant difference for the number of conks is not surprising considering that the fruiting of F. igniarius is dependent upon many factors (e.g. time since infection and genotype of the fungus) that are not related to the genetic constitution of the individual aspen clones.

Pearson correlation coefficients were determined to evaluate the possible linear relationships between the clonal tree characteristics and defect statistics in the six stands. Significant inverse relationships were obtained for natural pruning and percent stain in the Anthony Lake stand, and stub height and percent stain for the Stevens clones. Significant direct relationships were obtained for stub height and percent advanced rot (Kagiano Lake), stub height and percent stain (Anthony Lake), branch diameter and percent advanced rot (Fort Frances), and number of conks and percent advanced rot (Fort Frances and Stevens).

TABLE 5 Area means and the range in clone means for tree characteristics and the results of the analyses of variance

Characteristic	Area mean	Range: clone means	F-test sig.
		CAMP 15	
Natural pruning	2.1	1.7 - 2.6	**1
Stub height (m)	2.8	2.0 - 3.9	**
Branch diameter (cm)	2.1	1.7 - 2.8	**
Number of conks	0	0	--2
		RAMSEY LAKE	
Natural pruning	2.1	1.8 - 2.8	**
Stub height (m)	2.4	1.7 - 2.9	**
Branch diameter (cm)	2.6	2.0 - 3.3	**
Number of conks	0	0	--
		FORT FRANCES	
Natural pruning	2.3	1.8 - 2.8	**
Stub height (m)	2.7	1.7 - 3.6	**
Branch diameter (cm)	3.1	2.5 - 4.6	**
Number of conks	0.3	0 - 1.3	NS3
		KAGIANO LAKE	
Natural pruning	2.0	1.5 - 2.4	**
Stub height (m)	5.9	4.3 - 8.9	**
Branch diameter (cm)	4.4	2.9 - 5.4	**
Number of conks	0.1	0 - 0.4	NS
		STEVENS	
Natural pruning	2.0	1.3 - 2.6	**
Stub height (m)	7.3	5.0 - 12.3	**
Branch diameter (cm)	6.9	5.8 - 9.4	**
Number of conks	1.5	0 - 3.3	*4
		ANTHONY LAKE	
Natural pruning	1.7	1.2 - 2.6	**
Stub height (m)	10.2	6.2 - 13.2	**
Branch diameter (cm)	6.0	4.2 - 8.7	**
Number of conks	1.2	0.4 - 2.1	NS

1 - significant at the 0.01 level of probability
2 - not tested, no variation
3 - nonsignificant
4 - significant at the 0.05 level of probability

Site Factors and Defect

Correlations between the site factors and defect were determined for the 60 clone population and the individual stand populations. For the total population the best linear relationship would account for considerably less than 25% of the variation in the percent defect and its components. Within stand correlations for the defect variables and site factors were in some cases significant. As was suggested previously, the assumed importance of the selected site factors examined cannot be verified based upon the data, suggesting that other parameters may be more influential.

Site Effects on a Single Clone

A single large (.35 ha) clone in the Anthony Lake stand was divided into three portions based on apparent site differences, and sampled three times (clone 9, and plots 11 and 12). Analyses of variance for the dimension and defect statistics, and tree characteristics resulted in the detection of a highly significant difference for total height. Differences for the rest of the dimension statistics, and all of the defect and tree characteristic variables were statistically nonsignificant. The mean heights for the three samples were 28.4, 26.9 and 28.1 m, respectively. It appears that the suspected site differences among these three samples had little detectable influence on the growth of this genotype. For the most part, the site factors varied little in the three samples, so it is not surprising that only one significant difference was encountered. Linear relationships with such a small sample are of little value, however, there was a significant inverse linear relationship between height and the percent gravel in the B2 horizon. This is not to suggest that this is the only relationship or a causal relationship. For instance the basal area components (Total BA, Aspen BA and Aspen-suppressed Aspen BA) appear to have a nonlinear relationship with height. It may be that some factor, such as basal area, that expresses some measure of competition between trees is more closely related to height than any of the site factors.

Root Characteristics

Tests of interclonal variation for nine root characteristics were made by means of the analysis of variance for all ten clones in the Camp 15 and Ramsey Lake stands, and five clones in the Fort Frances stand (Table 6). In the Camp 15 sample significant variation was detected only for the number of sound large roots. The Ramsey Lake clones exhibited significant interclonal variation for seven of the nine root characteristics. Nonsignificant variation was detected only for total root collar rot (%) and the number of small roots. Root systems studied for five clones in the Fort Frances stand had significant interclonal variation for roots with stain (5), and roots with rot (%); all other characteristics exhibited nonsignificant variation. The fairly high occurrence of nonsignificant differences would suggest that there is little genetic variation in the characteristics examined. For the above ground portions of the trees it was suggested that a majority of the variation was the result of environmental factors, similarly variation of the root characteristics appears to be even more strongly influenced by environmental than genetic factors.

TABLE 6 Results of analysis of variance for the root characteristics

Characteristic	Camp 15	Ramsey Lake	Fort Frances
Total root collar stain (%)	NS1	*2	NS
Total root collar rot (%)	NS	NS	NS
Number of large roots	NS	*	NS
Number of sound large roots	*	**3	NS
Total large root stain (%)	NS	**	NS
Total large root rot (%)	NS	*	NS
Number of small roots	NS	NS	NS
Roots with stain (%)	NS	**	*
Roots with rot (%)	NS	*	*

1 - nonsignificant
2 - significant at the 0.05 level of probability
3 - significant at the 0.01 level of probability

Root Characteristics, and Dimension and Defect Statistics for Individual Trees

The magnitude and slope (+/-) of linear relationships between root characteristics, and dimension and defect statistics were determined using Pearson correlation. Of the 63 relationships examined, for the combined population (90 trees), only seven were significant (Table 7).

TABLE 7 Pearson correlation coefficients for root characteristics, and dimension and defect statistics that were significant

Statistic	Camp 15	Ramsey Lake	Fort Frances	Population
		NUMBER OF LARGE ROOTS		
Height	.49	.54	.88	.59
Dbh	.82	.83	.94	.89
Volume	.80	.82	.94	.78
		NUMBER OF SMALL ROOTS		
Dbh	.37	.62	.63	.34
		TOTAL ROOT COLLAR STAIN (%)		
% Defect	.32	.35	--	.24
% Stain	--	.35	--	.22
		TOTAL ROOT COLLAR ROT (%)		
% Incipient rot	--	.33	.75	.25

For the dimension statistics, height, dbh and volume (i.b.) were positively related with the number of large roots, and dbh was positively related to the number of small roots. Defect statistics were directly correlated to root characteristics in the following combinations: percent defect and total root collar stain (%), percent incipient rot and total root collar rot (%), and percent stain and root collar stain (%). Of the significant relationships for the combined population, only four were also significant for the three subsets of the population. Dbh was directly related to the number of small roots, and height, dbh and volume (i.b.) were directly related to the number of large roots. The positive correlation between dbh and the number of large roots varies the least at any level in the population, and the linear trend would account for at least 67% of the variation encountered in the sample population. Accounts of such a relationship in aspen are lacking in the literature, but it does confirm to a degree what one would logically expect that large stems would tend to have more roots than smaller stems.

SUMMARY AND CONCLUSIONS

Cultures of defective (stained or decayed) stem wood revealed the presence of micro-organisms (bacteria and/or fungi) in all of the 800 trees sampled. The fungi that decay wood are the most important of these organisms and belong to the Order Hymenomycetales. Seventeen species of Hymenomycetes were identified from the cultures, and of these four species (Peniophora polygonia, Fomes igniarius, Armillaria mellea and Radulum casearium) were isolated with some regularity. The frequency of occurrence for Hymenomycetes, and of decay, tended to increase with stand age. The occurrence of P. polygonia genotype, or an interaction of the two. The other three major wood decay fungi exhibited positive linear trends with age. Similar differences in occurrence for these organisms between the Fort Frances stand and the Terrace Bay stands could not be evaluated, due to their low occurrence in the young (≈30 year) stands.

Significant interclonal differences within a stand for the occurrence of Hymenomycetes were infrequent, although significant differences among the stands for groups of trees were detected for 10 of the fungi. The differences among stands are in most cases attributable to age differences. Interclonal differences in occurrence suggest the possibility of resistance mechanisms; however, with such an ecologically complex system (environmental differences within the stand and host-pathogen relationship) and passive resistance systems the possibility of finding simple genotypic resistance seems remote.

Interclonal variation was highly significant ($p<0.01$) in all stands for total height, diameter breast height, volume (i.b.), percent bark, percent defect, percent stain, natural pruning, stub height, and branch diameter, while the significance of interclonal variation for the percent advanced rot, percent incipient rot, and number of conks varied ($p<0.05$, $p>0.5$, and $p<.01$) from stand to stand. The consistent significant interclonal variation for the six dimension and defect statistics, and the three tree characteristics listed, suggests that the genetic constitution of the clones contributes significantly to the observed variation.

Broad sense heritability estimates suggest that on the average less than one-third of the variation was the result of genetic constitution, except for total height ($h^2 = 0.58$), percent stain ($h^2 = 0.39$), and stub

height (h^2 = 0.37). Buijtenen, et al. (1959) suggested that selection in aspen for growth characteristics would result in little gain, and Zahner and Crawford (1965) thought that trembling aspen was more influenced by site and topographic factors than bigtooth aspen (Populus grandidentata Michx.). The results of this study also suggest that only small gains could be made by selecting for growth and defect statistics, and tree characteristics; and that environmental factors play the more important role in the observed phenotypic variation.

Correlations, within stands, between the defect statistics, and the growth statistics, tree characteristics and the site factors were mostly nonsignificant. This suggests that defect and its component parts were probably independent of the other variables considered. Graphically it was observed that the percent defect was related to the position of the clones with respect to a main haul road in two of the stands and not the measured site characteristics suggesting that other environmental factors (micro-climate) may be more important.

The effects of site on the dimension and defect statistics, and on the tree characteristics, were evaluated for a single clone in the Anthony Lake stand that covered three topographic areas recognized as being different sites. Analysis of variance revealed that the only significant difference occurred for total height. Site factors varied little between the three areas and it was suggested that the site factors were perhaps not the most strongly related variables, or causal, of the observed differences.

Interclonal variation for the root characteristics studied was mostly nonsignificant. Only in the Ramsey Lake stand was there appreciable variation detected. The general lack of significant variation suggests that genetic variation of these factors is very much limited compared to the environmental effects.

Correlations between the root characteristics, and the dimension and defect statistics were mostly nonsignificant for the stems (90 trees) examined. The most consistent correlation was the significant positive relationship between dbh and the number of large roots for any subset of the population.

The results of this study indicate that the development of a clonal management system based upon the available information would achieve less than the development of silvicultural techniques to improve the growth and reduce the defect of aspen stands, based upon the apparent amount of variation due to environmenal variables that have yet to be positively defined.

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